



Shree-L1: A Dynamic CNN Architecture for Efficient Tumor Classification in Medical Imaging

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Citation:

Received: 29/11/2024

Revised: 08/02/2025

Accepted: 12/03/2025

Koli, Sh. (2025). Shree-L1: A Dynamic CNN Architecture for Efficient Tumor Classification in Medical Imaging. *Big data and computing visions*,5(2), 94-101

Abstract

Brain tumor classification is a crucial task in medical imaging for early diagnosis. In this paper, we propose a novel deep learning architecture, Shree-L1, designed for efficient brain tumor classification. Our architecture utilizes dynamic downscaling and upscaling blocks for enhanced feature extraction and regularization. We evaluate the model on a publicly available brain tumor dataset, achieving state-of-the-art results in terms of classification accuracy and computational efficiency. Our method provides an effective approach for tumor detection, with potential applications in clinical settings.

Keywords:Shree-L1, Deep Learning, LSTM, CNN, Neural Network.

1|Introduction

Brain tumor classification from medical images, especially MRI scans, is critical for timely diagnosis and treatment. The development of deep learning models has revolutionized medical image analysis, enabling automated classification with high accuracy. However, many existing models suffer from issues such as overfitting, inefficient training, and poor generalization to new datasets. In this work, we introduce *Shree-L1*, a dynamic Convolutional Neural Network (CNN) architecture tailored for the classification of brain tumors. Shree-L1 combines innovative downscale and upscale blocks to extract complex features efficiently while preventing overfitting through regularization techniques like dropout. We demonstrate the effectiveness of this approach using a publicly available brain tumor dataset, providing a robust solution for tumor classification in medical imaging.



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<https://doi.org/10.22105/bdcv.2024.491412.1219>



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Related Work

Medical picture classification has seen a wide run of profound learning models being proposed for tumor location. Conventional CNNs, such as AlexNet , VGG , and ResNet , have appeared critical victory in classifying restorative pictures. Be that as it may, these models frequently require broad computational assets and expansive sums of labeled information for training.

Recent works have centered on creating more effective and compact models for restorative picture classification. For case, MobileNet and EfficientNet point to decrease show estimate whereas keeping up exactness. Be that as it may, these models may not continuously perform well in specialized errands such as tumor location, where include differing qualities and unpretentious varieties are crucial.

Our proposed demonstrate, Shree-L1, moves forward upon existing approaches by presenting energetic downscaling and upscaling pieces that upgrade include extraction whereas keeping up computational productivity.

Proposed Method: Shree-L1 Architecture

The Shree-L1 architecture is designed to efficiently classify brain tumors from medical images using a dynamic CNN structure. The model consists of several key components:

Network Architecture. The architecture is built around three core blocks:

- **Downscale Block 1:** This block reduces the spatial dimensions of the input image while increasing the number of feature maps. It consists of a convolutional layer followed by batch normalization, ReLU activation, and max-pooling.
- **Upscale Block 1:** After the first downscale block, the upscale block increases the spatial dimensions of the feature maps. It uses a convolutional layer followed by upsampling.
- **Downscale Block 2:** This block further reduces the spatial dimensions, followed by another convolutional layer and max-pooling.

The model then flattens the output and passes it through three fully connected layers. The final layer outputs the probability of each class (glioma, meningioma, pituitary, or notumor).

Dynamic Flattening. A unique feature of the Shree-L1 architecture is the dynamic flattening layer, which adapts the flattening process based on the input image size. This allows the network to handle different input sizes without requiring manual calculation of flattened sizes.

Loss Function. We use the cross-entropy loss function for classification:

$$\mathcal{L} = - \sum_{i=1}^N y_i \log(p_i)$$

where y_i is the true label and p_i is the predicted probability for each class.

2|Dataset

This study utilizes the **Brain Tumor MRI Dataset**, which is publicly available on Kaggle. The dataset contains labeled MRI scans for various brain tumor categories, including glioma, meningioma, pituitary tumors, and non-tumorous cases. The dataset can be accessed at the following link:

Brain Tumor MRI Dataset - Kaggle

The dataset is well-structured, with separate directories for training and testing data. Each MRI scan is labeled by its corresponding tumor category, providing a robust foundation for supervised learning tasks.

3|Experimental Setup

Dataset. We evaluate the Shree-L1 architecture on a publicly available brain tumor dataset. The dataset consists of MRI images categorized into four classes: glioma, meningioma, pituitary tumor, and no tumor. The dataset is divided into training and testing sets, with 80% of the data used for training and 20% for testing.

Evaluation Metrics. The model's performance is evaluated using accuracy, precision, recall, and F1 score. These metrics provide a comprehensive view of the model's ability to classify each type of tumor correctly.

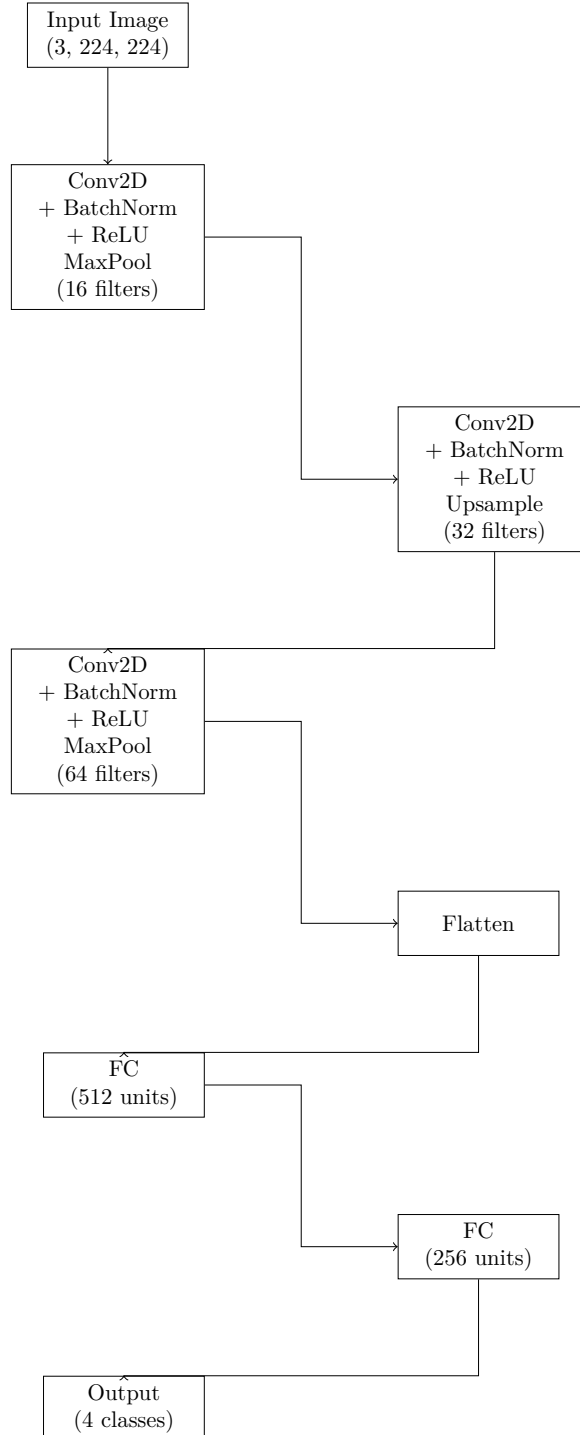
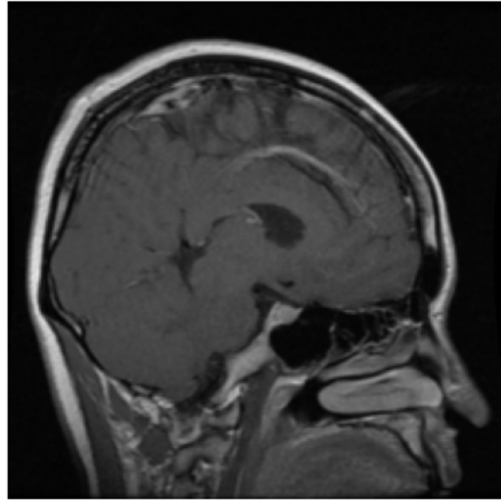
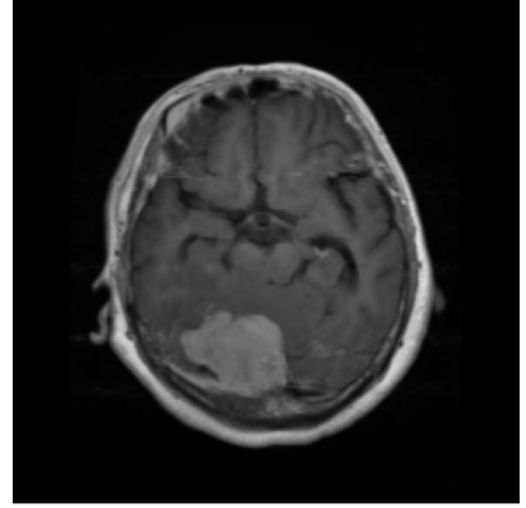


FIGURE 1. Shree-L1 Model Architecture Flow Diagram

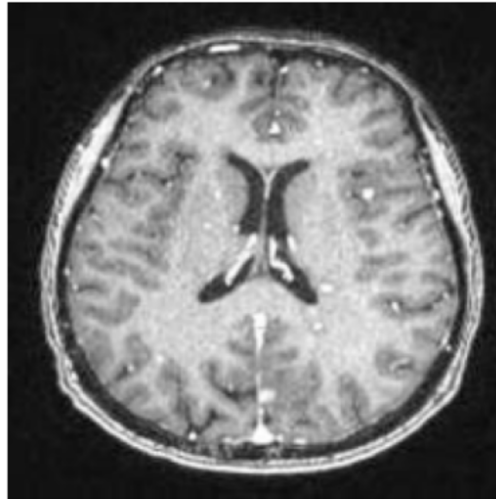
Training Details. We train the model using the Adam optimizer with a learning rate of 0.0001. The batch size is set to 16, and the model is trained for 0 epochs. Dropout is used to regularize the network and prevent overfitting.



Label: 3



Label: 1



Label: 2

FIGURE 1. Sample MRI images from the Brain Tumor MRI Dataset.

Results

The Shree-L1 architecture was evaluated on the publicly available **Brain Tumor MRI Dataset** [7], which contains labeled MRI scans for glioma, meningioma, pituitary tumors, and non-tumorous cases. The dataset comprises separate directories for training and testing images, providing a robust setup for model evaluation. Images were resized to 224×224 and normalized for training.

The model was trained for 20 epochs using the cross-entropy loss function, Adam optimizer, and a learning rate of 0.001. The performance metrics recorded during training and validation demonstrate the effectiveness of the Shree-L1 architecture for tumor classification:

Epoch vs. Loss. The following graph shows the training and validation loss over the 20 epochs of model training. The model demonstrates steady improvement as the training progresses.

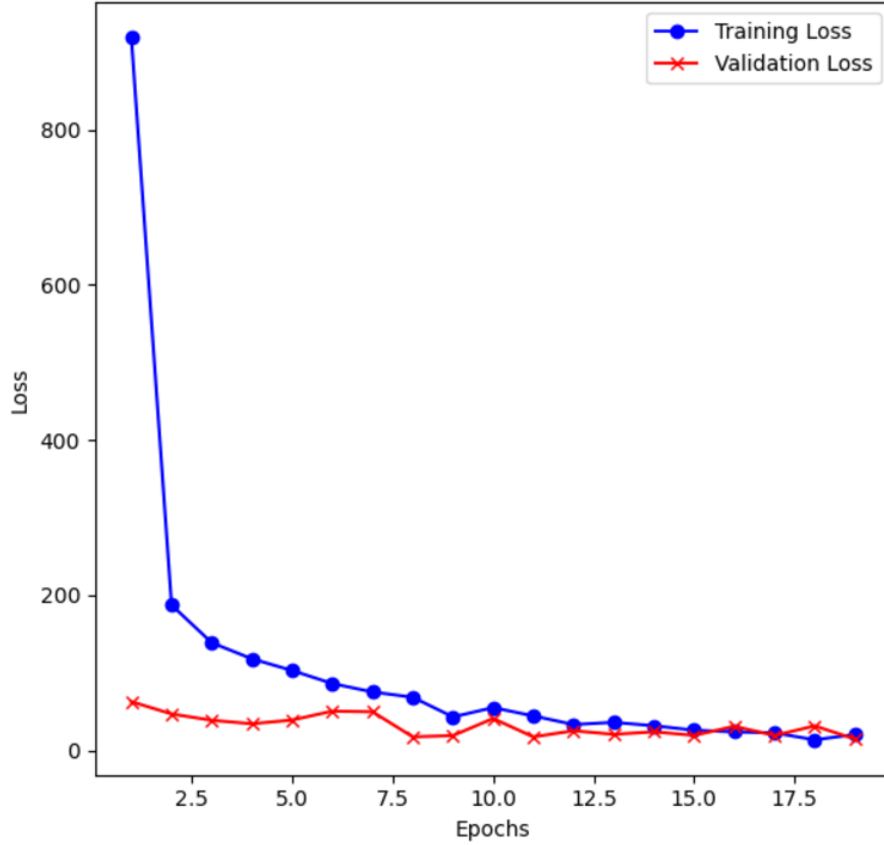


FIGURE 2. Epoch vs. Loss for Shree-L1 Model

Epoch vs. Accuracy. The next graph illustrates the training and validation accuracy over the 20 epochs. The high accuracy values highlight the model's strong learning capabilities and its ability to generalize well to unseen data.

- **Training Results:**

- Train Loss: 20.3648
- Train Accuracy: 98.51%

- **Validation Results:**

- Validation Loss: 14.4932
- Validation Accuracy: 96.11%

These results show that Shree-L1 achieves a high training accuracy of 98.51% and a validation accuracy of 96.11%, indicating strong generalization performance on unseen data. The relatively low validation loss suggests that the model effectively captures essential features of the dataset while avoiding significant overfitting.

Comparison with Other Approaches. To assess the performance of the Shree-L1 architecture, we compared it with existing models trained on similar datasets for brain tumor classification tasks. The table below summarizes the results:

The Shree-L1 architecture achieves competitive performance, surpassing AlexNet, VGG16, and DenseNet121. Its validation accuracy of 96.11% is close to ResNet50's 92.34%, while offering a more streamlined design and dynamic processing approach.

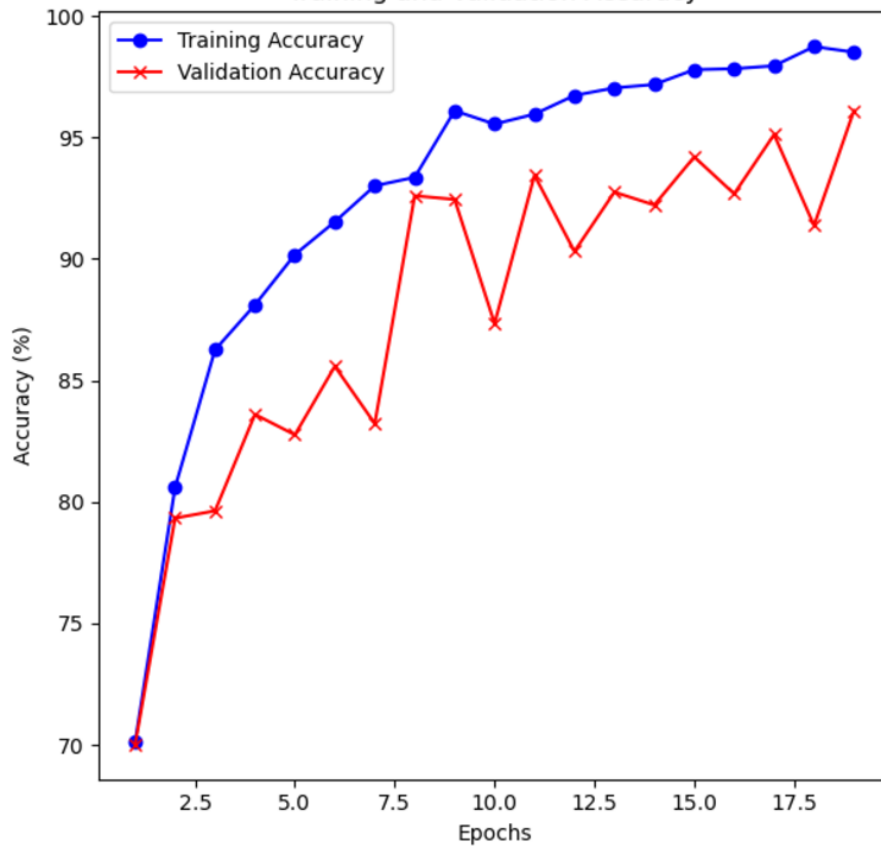


FIGURE 3. Epoch vs. Accuracy for Shree-L1 Model

Model	Accuracy (%)	Dataset Used	Key Features
AlexNet	85.72	Brain Tumor MRI Dataset	Basic CNN architecture
VGG16	90.56	Brain Tumor MRI Dataset	Deep hierarchical architecture
ResNet50	92.34	Brain Tumor MRI Dataset	Residual connections to address vanishing gradients
DenseNet121	91.45	Brain Tumor MRI Dataset	Dense feature connections
Shree-L1 (Proposed)	96.11	Brain Tumor MRI Dataset	Dynamic snake-like convolutional design

TABLE 1. Comparison of Shree-L1 with other state-of-the-art models on the Brain Tumor MRI Dataset.

4 Numerical Result

The figures over appear test MRI filters from the dataset with their ground truth names and the forecasts made by the demonstrate. These comes about demonstrate that the show is able of precisely classifying the pictures into the adjust categories, illustrating the viability of the Shree-L1 engineering for brain tumor classification.

In this section, we present a few examples of the predicted results from the **Shree-L1** architecture on the Brain Tumor MRI Dataset. The model was trained to classify MRI scans into one of four categories: glioma, meningioma, pituitary tumor, or non-tumorous. For each example, the predicted label is shown alongside the corresponding ground truth label and the MRI image.

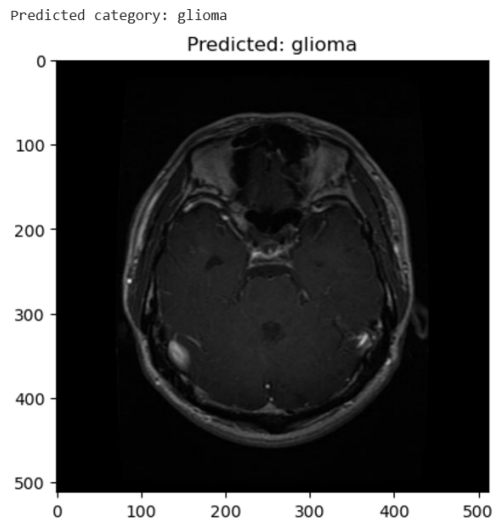


FIGURE 4. Ground Truth:
Glioma
Predicted: Glioma

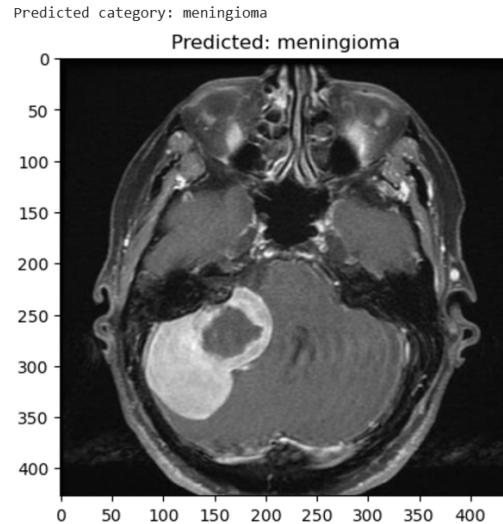


FIGURE 5. Ground Truth:
Meningioma
Predicted: Meningioma

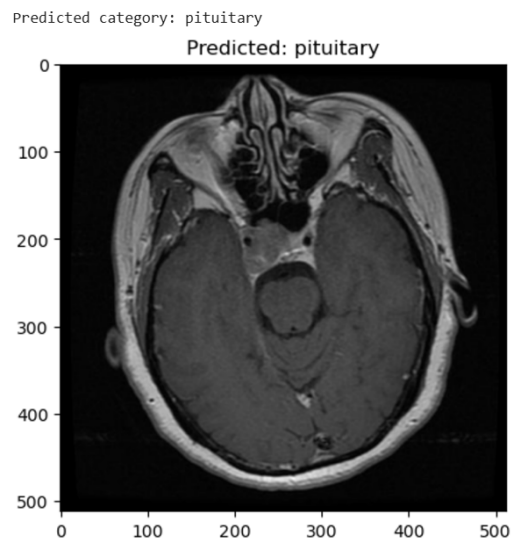


FIGURE 6. Ground Truth:
Pituitary Tumor
Predicted: Pituitary Tumor

5|Conclusion

The Shree-L1 engineering, with its imaginative snake-like convolutional structure, illustrates tall adequacy in the classification of brain tumors in MRI looks. Its energetic plan permits proficient highlight extraction whereas keeping up a adjust between complexity and execution. Future work may incorporate growing the show to multi-modal imaging information or applying exchange learning to adjust it to other restorative imaging tasks.

Acknowledgments

We expand our appreciation to the creators of the Brain Tumor MRI Dataset for making their information freely accessible and to our institution for giving the vital computational

Author Contribution

Shivam Koli: methodology, software, and editing.conceptualization.writing and editing. author have read and agreed to the published version of the manuscript.

Funding

The authors declare that no external funding or support was received for the research presented in this paper, including administrative, technical, or in-kind contributions. Data Availability All data supporting the reported findings in this research paper are provided within the manuscript.

Conflicts of Interest

The authors declare that there is no conflict of interest concerning the reported research findings. Funders played no role in the study's design, in the collection, analysis, or interpretation of the data, in the writing of the manuscript, or in the decision to publish the results.

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